In the Specification:

On page 6 at line 17, please replace the present paragraph with the following paragraph:

--The present invention provides recombinant host cells and expression vectors for making products in host cells, which are otherwise unable to make those products due to the lack of a biosynthetic pathway to produce a precursor required for biosynthesis of the product. As used herein, the term recombinant refers to a cell, compound, or composition produced at least in part by human intervention, particularly by modification of the genetic material of a cell. The present invention also provides methods for increasing the amounts of a product produced in a host cell by providing recombinant biosynthetic pathways for production of a precursor utilized in the biosynthesis of a product.--

On page 56 at line 15, please replace the present paragraph with the following paragraph:

--To express active mutase *in vivo*, it was necessary to grow cells in a defined media (MUT media) that allows uptake of the vitamin B12 precursor hydroxocobalamin; this is similar to an established protocol for expression of active methionine synthase, which also requires B12. Cell extracts overexpressing the mutase were shown to convert mm-CoA to succinyl CoA without the addition of vitamin B12. Only one time point (at 20 minutes) was assayed to confirm activity; the specific activity of the mutase was not determined.--

On page 56 at line 22, please replace the present paragraph with the following paragraph:

--Thus, methylmalonyl-CoA mutase was expressed as the active holoenzyme in *E. coli*, and methylmalonyl-CoA was produced in vivo. Because a slow, spontaneous chemical epimerization between (R)- and (S)-mm-CoA does exist (approximately 3% in 15 minutes), it may be helpful to determine the relative amounts of these diastereomers

in cells overexpressing the mutase. Enough (S)-mm-CoA may be present to support polyketide production in some cells without addition of an epimerase. To facilitate the eventual production of polyketides in *E. coli,* the mutase gene can be incorporated into the chromosome of the BL21 *panD* cell or other host cell.--

On page 69 line 26, please replace the present paragraph with the following paragraph:

--Epimerase activity was measured in crude extracts of *E. coli* harboring either pET-epsherm, pET-epcoel, pET-epsub, or a control pET vector. The epimerase assay couples transcarboxylase, which converts (S)-methylmalonyl-CoA into propionyl-CoA, to malate dehydrogenase, which converts NADH into NAD^+, producing a decrease in absorbance at 340 nm. The assay is initiated with a racemic mixture of (R,S)-methylmalonyl-CoA; when the (S)-isomer is consumed as described below, a steady background rate is observed at about one-tenth of the initial rate. When an extract containing epimerase is added to the assay, the (R)-isomer is converted to (S)-, resulting in a further decrease in absorbance. In crude *E. coli* extracts, however, a significant background rate is observed, probably due to an endogenous NADH oxidase. Thus the epimerase must be expressed at a sufficiently high level to conclude that it is active. The assay was conducted as follows.--

On page 73 line 28, please replace the present paragraph with the following paragraph:

--Most modular PKSs require either or both malonyl-CoA or (2*S*)-methylmalonyl-CoA as a source of 2-carbon units for polyketide biosynthesis. The malonyl-CoA pools in yeast are quite sufficient for polyketide synthesis, as illustrated by the production of large amounts of 6-MSA in yeast. However, *S. cerevisiae* does not produce (2*S*)-methylmalonyl-CoA and does not possess biosynthetic pathways for methylmalonyl-CoA biosynthesis. Hence, a heterologous biosynthetic pathway must be

introduced into *S. cerevisiae* to support biosynthesis of polyketides that use (2S)-methylmalonyl-CoA as a precursor. --

On page 82 line 11, please replace the present paragraph with the following paragraph:

--As described in Example 1, methylmalonyl-CoA epimerase was purified from *Propionibacterium shermanii* and N-terminal and internal protein sequence was obtained. Degenerate PCR primers based on the amino acid sequences were designed and were used to amplify a 180 bp PCR product from *P. shermanii* genomic DNA. The PCR product was labeled and used to isolate the epimerase gene from *P. shermanii*. The methylmalonyl-CoA epimerase genes from *B. subtilis* [16] and *S. coelicolor* can also be employed in the methods of the present invention.--

On page 83 line 1, please replace the present paragraph with the following paragraph:

--Propionyl-CoA is not detected in *E. coli* SJ16 cells grown in the presence of [^{3}H] ß-alanine with or without the addition of propionate in the growth media. When *E. coli* SJ16 cells were transformed with a pACYC-derived plasmid containing the *Salmonella typhimurium* propionyl-CoA ligase gene (*prpE)* under the control of the *lac* promoter, a small amount of propionyl-CoA was observed (~0.2% of total CoA pool) in cell extracts. When 5 mM sodium propionate was included in the culture medium, about 14-fold more propionyl-CoA was produced (~3% of the total CoA pool). --